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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/767,597

DATE: 12/19/2001
TIME: 13:23:59

Input Set : N:\Crf3\RULE60\09767597.txt
Output Set: N:\CRF3\12192001\I767597.raw

3 <110> APPLICANT: Jegla, Timothy James
4 ICAgen, Inc.
6 <120> TITLE OF INVENTION: Human HAC3
8 <130> FILE REFERENCE: 018512-002210US
10 <140> CURRENT APPLICATION NUMBER: 09/767,597
11 <141> CURRENT FILING DATE: 2001-01-22
13 <150> PRIOR APPLICATION NUMBER: 09/548,933
14 <151> PRIOR FILING DATE: 2000-04-13
16 <160> NUMBER OF SEQ ID NOS: 16
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 774
22 <212> TYPE: PRT
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <223> OTHER INFORMATION: human hyperpolarization-activated voltage-gated
27 cation channel 3 (HAC3)
29 <400> SEQUENCE: 1
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31 1 5 10 15
33 Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala
34 20 25 30
36 Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His
37 35 40 45
39 Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val
40 50 55 60
42 Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser
43 65 70 75 80
45 Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp
46 85 90 95
48 Asp Leu Ile Met Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro
49 100 105 110
51 Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val
52 115 120 125
54 Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn
55 130 135 140
57 Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala
58 145 150 155 160
60 Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp
61 165 170 175
63 Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu
64 180 185 190
66 Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg
67 195 200 205
69 Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu
70 210 215 220
72 Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met

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73	225	230	235	240
75	Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly			
76	245	250	255	
78	Met Met Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val			
79	260	265	270	
81	Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His			
82	275	280	285	
84	Met Val Asn His Ser Trp Gly Arg Gln Tyr Ser His Ala Leu Phe Lys			
85	290	295	300	
87	Ala Met Ser His Met Leu Cys Ile Gly Tyr Gly Gln Gln Ala Pro Val			
88	305	310	315	320
90	Gly Met Pro Asp Val Trp Leu Thr Met Leu Ser Met Ile Val Gly Ala			
91	325	330	335	
93	Thr Cys Tyr Ala Met Phe Ile Gly His Ala Thr Ala Leu Ile Gln Ser			
94	340	345	350	
96	Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu Lys Tyr Lys Gln Val Glu			
97	355	360	365	
99	Gln Tyr Met Ser Phe His Lys Leu Pro Ala Asp Thr Arg Gln Arg Ile			
100	370	375	380	
102	His Glu Tyr Tyr Glu His Arg Tyr Gln Gly Lys Met Phe Asp Glu Glu			
103	385	390	395	400
105	Ser Ile Leu Gly Glu Leu Ser Glu Pro Leu Arg Glu Glu Ile Ile Asn			
106	405	410	415	
108	Phe Thr Cys Arg Gly Leu Val Ala His Met Pro Leu Phe Ala His Ala			
109	420	425	430	
111	Asp Pro Ser Phe Val Thr Ala Val Leu Thr Lys Leu Arg Phe Glu Val			
112	435	440	445	
114	Phe Gln Pro Gly Asp Leu Val Val Arg Glu Gly Ser Val Gly Arg Lys			
115	450	455	460	
117	Met Tyr Phe Ile Gln His Gly Leu Leu Ser Val Leu Ala Arg Gly Ala			
118	465	470	475	480
120	Arg Asp Thr Arg Leu Thr Asp Gly Ser Tyr Phe Gly Glu Ile Cys Leu			
121	485	490	495	
123	Leu Thr Arg Gly Arg Arg Thr Ala Ser Val Arg Ala Asp Thr Tyr Cys			
124	500	505	510	
126	Arg Leu Tyr Ser Leu Ser Val Asp His Phe Asn Ala Val Leu Glu Glu			
127	515	520	525	
129	Phe Pro Met Met Arg Arg Ala Phe Glu Thr Val Ala Met Asp Arg Leu			
130	530	535	540	
132	Leu Arg Ile Gly Lys Lys Asn Ser Ile Leu Gln Arg Lys Arg Ser Glu			
133	545	550	555	560
135	Pro Ser Pro Gly Ser Ser Gly Gly Ile Met Glu Gln His Leu Val Gln			
136	565	570	575	
138	His Asp Arg Asp Met Ala Arg Gly Val Arg Gly Arg Ala Pro Ser Thr			
139	580	585	590	
141	Gly Ala Gln Leu Ser Gly Lys Pro Val Leu Trp Glu Pro Leu Val His			
142	595	600	605	
144	Ala Pro Leu Gln Ala Ala Val Thr Ser Asn Val Ala Ile Ala Leu			
145	610	615	620	

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147 Thr His Gln Arg Gly Pro Leu Pro Leu Ser Pro Asp Ser Pro Ala Thr
148 625 630 635 640
150 Leu Leu Ala Arg Ser Ala Trp Arg Ser Ala Gly Ser Pro Ala Ser Pro
151 645 650 655
153 Leu Val Pro Val Arg Ala Gly Pro Trp Ala Ser Thr Ser Arg Leu Pro
154 660 665 670
156 Ala Pro Pro Ala Arg Thr Leu His Ala Ser Leu Ser Arg Ala Gly Arg
157 675 680 685
159 Ser Gln Val Ser Leu Leu Gly Pro Pro Pro Gly Gly Gly Arg Arg
160 690 695 700
162 Leu Gly Pro Arg Gly Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro
163 705 710 715 720
165 Gln Arg Ala Thr Gly Asp Gly Ser Pro Gly Arg Lys Gly Ser Gly Ser
166 725 730 735
168 Glu Arg Leu Pro Pro Ser Gly Leu Leu Ala Lys Pro Pro Arg Thr Ala
169 740 745 750
171 Gln Pro Pro Arg Pro Pro Val Pro Glu Pro Ala Thr Pro Arg Gly Leu
172 755 760 765
174 Gln Leu Ser Ala Asn Met
175 770
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 2325
180 <212> TYPE: DNA
181 <213> ORGANISM: Homo sapiens
183 <220> FEATURE:
184 <223> OTHER INFORMATION: human hyperpolarization-activated voltage-gated
185 cation channel 3 (HAC3)
187 <400> SEQUENCE: 2
188 atggaggca ggcacggcc ggcggcgaaa gcccacggcc tggactggag 60
189 gcggtgcctc ccgttgcgtcc cccgcctgcg accgcggccct cagggtccgat ccccaatct 120
190 gggcctgagc ctaagaggag gcaccttggg acgtgtgtcc agcctacggt caacaagttc 180
191 tcccttcggg tggccggcag ccacaaagca gtggaaatcg agcaggagcg ggtgaagtca 240
192 gccccggccct ggatcatcca cccctacagc gacttccgggt tttactgggaa cctgtatcatg 300
193 ctgtctgtca tgggtgggaa cctcatgtc ctgcgtgtgg gcatcacctt cttcaaggag 360
194 gagaactccc cgccttggat cgtcttcaac gtattgtctg atactttctt cctactggat 420
195 ctgggtgtca acttccgaac gggcatgtc gtggaggagg gtgctgagat cctgctggca 480
196 cccggggccca tccgcacgcg ctacctgcgc acatgggtcc tgggtgacccatcatctt 540
197 atccctgtgg attacatctt octagtggtt gagctggagc cacgggttggc cgctgaggatc 600
198 tacaaaacgg cacggccct acgcacatgtt cgcttcacca agatcctaag cctgctgagg 660
199 ctgtccgcct tctccgcct catccgtac atacaccgtt gggaggagat ctttcacatg 720
200 acctatgacc tggcaagtgc tgggttgcg atcttcaacc tcattggat gatgctgtc 780
201 ctatgtcaact gggatggctg tctgcagttc ctgggtccca tgctgcagga cttccctccc 840
202 gactgctggg tctccatcaa ccacatgggtt aaccactcgat gggggccgcgtt gtattccat 900
203 gcccgttca aggccatgag ccacatgtc tgcatggct atgggcagca ggcacccgtt 960
204 ggcacatggcc acgttgcgtt caccatgtc agcatgtatcg taggtgcacatgtacggcc 1020
205 atgttcatcg gccatgccac ggcactcatc cagttccgtt actcttcccg gcgtcagttac 1080
206 caggagaagt acaaggcaggat ggagcagttac atgttccatcc acaagctgccc agcagacacg 1140
207 cggcagcgtca tccacagatc ctatgagcac cgctaccagg gcaagatgtt cgatgaggaa 1200
208 agcatcctgg cgagcttagt cgagccgtt cgcgaggaga tcattaaactt caccgtcg 1260

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209 ggcctggtgg cccacatgcc gctgtttgcc catgccgacc ccagcttcgt cactgcagtt 1320
210 ctcaccaagc tgcgcgttga ggtcttccag ccgggggatc tcgtgggtcg tgagggctcc 1380
211 gtggggagaga agatgtactt catccagcat gggctgctca gtgtgctggc ccgcggcgcc 1440
212 cgggacacac gcctcaccga tggatcctac tttggggaga tctgcctgt aactaggggc 1500
213 cggcgcacag ccagtgttcg ggctgacacc tactgccgc tttactcaact cagcgtggac 1560
214 catttcaatg ctgtgcttga ggagttcccc atgatgcgc gggccttga gactgtggcc 1620
215 atggatcggc tgctccgcat cggcaagaag aattccatac tgcagcggaa gcgcctccgag 1680
216 ccaagtccag gcagcagtgg tggcatcatg gagcagcaact tggtgcaaca tgacagagac 1740
217 atggctcggg gtgttcgggg tcggggccccc agcacaggag ctcaagcttag tgaaaagcca 1800
218 gtactgtggg agccactggt acatgcgc cttcaggcag ctgctgtgac ctccaatgtg 1860
219 gccattgccc tgactcatca gcggggccct ctgcccctct cccctgactc tccagccacc 1920
220 ctccctgctc gctctgttt ggcgtcagca ggctctccag ctcccccgct ggtgcccgtc 1980
221 cgagctggcc catgggcatac cacctcccgcc ctgcccggcc cacctggccg aaccctgcac 2040
222 gccagcctat cccgggcagg ggcgtcccgat gtctccctgc tgggtcccccc tccaggagga 2100
223 ggtggacggc ggcttaggacc tcggggccgc ccaactctcag ctcccccaacc ctctctgcct 2160
224 cagcggcaca caggcgatgg ctctcctggg cgttaaggat caggaagtga gcggctgcct 2220
225 ccctcagggc tcctggccaa acctccaagg acagcccagc ccccccaggcc accagtgcct 2280
226 gagccagcca caccccgggg tctccagctt tctgccaaca tgtaa 2325
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230 <211> LENGTH: 24
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Description of Artificial Sequence:amplification
236 primer
238 <400> SEQUENCE: 3
239 cagccatgga ggcagagcag cggc 24
242 <210> SEQ ID NO: 4
243 <211> LENGTH: 28
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence:amplification
249 primer
251 <400> SEQUENCE: 4
252 ggaggagatc tttcacatga catacgac 28
255 <210> SEQ ID NO: 5
256 <211> LENGTH: 24
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Description of Artificial Sequence:amplification
262 primer
264 <400> SEQUENCE: 5
265 agtaggatcc atcggtgagg cgtg 24
268 <210> SEQ ID NO: 6
269 <211> LENGTH: 27
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence

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273 <220> FEATURE:
 274 <223> OTHER INFORMATION: Description of Artificial Sequence:amplification
 275 primer
 277 <400> SEQUENCE: 6
 278 ttacatgttgcagaaagctggagacc 27
 281 <210> SEQ ID NO: 7
 282 <211> LENGTH: 29
 283 <212> TYPE: DNA
 284 <213> ORGANISM: Artificial Sequence
 286 <220> FEATURE:
 287 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
 288 amplification primer
 290 <220> FEATURE:
 291 <221> NAME/KEY: modified_base
 292 <222> LOCATION: (24)
 293 <223> OTHER INFORMATION: n = g, a, c or t
 295 <400> SEQUENCE: 7
 W--> 296 tgggaggaga tcttcayat gacntayga 29
 299 <210> SEQ ID NO: 8
 300 <211> LENGTH: 27
 301 <212> TYPE: DNA
 302 <213> ORGANISM: Artificial Sequence
 304 <220> FEATURE:
 305 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
 306 amplification primer
 308 <220> FEATURE:
 309 <221> NAME/KEY: modified_base
 310 <222> LOCATION: (16)
 311 <223> OTHER INFORMATION: n = g, a, c or t
 313 <220> FEATURE:
 314 <221> NAME/KEY: modified_base
 315 <222> LOCATION: (25)
 316 <223> OTHER INFORMATION: n = g, a, c or t
 318 <400> SEQUENCE: 8
 W--> 319 cgtctcgaat gccccknckca tcatngg 27
 322 <210> SEQ ID NO: 9
 323 <211> LENGTH: 26
 324 <212> TYPE: DNA
 325 <213> ORGANISM: Artificial Sequence
 327 <220> FEATURE:
 328 <223> OTHER INFORMATION: Description of Artificial Sequence:first round 5'
 329 RACE gene specific primer
 331 <400> SEQUENCE: 9
 332 cctgctgcccatagccaaatgcacagc 26
 335 <210> SEQ ID NO: 10
 336 <211> LENGTH: 25
 337 <212> TYPE: DNA
 338 <213> ORGANISM: Artificial Sequence
 340 <220> FEATURE:

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/767,597

DATE: 12/19/2001
TIME: 13:24:00

Input Set : N:\Crf3\RULE60\09767597.txt
Output Set: N:\CRF3\12192001\I767597.raw

L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8